SEQUENCE LISTING

GENERAL INFORMATION:

APPLICANT
NAME: Cheil Jedang Corporation
STREET:
CITY: Seoul
COUNTRY: Republic of Korea
POSTAL CODE (ZIP): 100-095
TELEPHONE: 82 2 7268 286
TELEFAX: 82 2 7268 219
TELEX:

Sub A1
7

TITLE OF INVENTION: Trehalose Synthase/Protein, Gene, Plasmids, Microorganisms, and A Process for Producing Trehalose

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:
ADDRESS: 500, 5-ga, Namdaemun-ro, Chung-ku
STREET:
CITY: Seoul
STATE OR PROVINCE:
COUNTRY: Republic of Korea
POSTAL CODE: 100-095

COMPUTER READABLE FORM:
MEDIUM TYPE : Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Notepad, Hangul 97

CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
COUNTRY: Republic of Korea
APPLICATION NUMBER:

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FILING DATE:
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Choi, Hak Hyun and Hwang, Ju Myung
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:
TELEPHONE: 82 2 365 2727
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INFORMATION FOR SEQ ID NO: 1

SEQUENCE CHARACTERISTICS:
LENGTH: 4753
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

MOLECULE TYPE: Trehalose Synthase Gene

HYPOTHETICAL:

ANTI-SENSE:

ORIGINAL SOURCE:
ORGANISM: Pseudomonas stutzeri
STRAIN: CJ38

SEQUENCE DESCRIPTION: SEQ ID NO: 1

GATCGCTGGC GTACTGCAGG TAGAGCAGGC GCATCGGCCC CCAGGGCGCA TCGGCCGGCT 60
CCGCTGTGCC CTGCTGGTTC ATGAAGCGGA CGAAGCGGCC ATCGCGGAAC CGTGGACGCC 120
ATTCGGGGCT GTCCGGGTCG CGGCTGTCGG TGAGCGTGCG CCACAGGTCG CTGCGAAACG 180
GCGGACCGCT CCAAAGCGCG CCGTGGATGG GATCGCCGAG CAGTTCGTGC AGCTCCCAGG 240
AACGTTGCGA ATGCAGCGCG CCGAGGCTCA GGCCATGCAG ATACAGGCGC GGTCGGCGTT 300
CGGCCGGCAG TTCGGTCCAG TAGCCATAGA TCTCGGCGAA TAGCGCGCGG GCCACGTCGC 360
GGCCGTAGTC GGCCTCCACC AGCAGCGCCA GCGGGCTGTT CAGATAGGAG TACTGCAACG 420
CCACGCTGGC GATATCGCCG TGGTGCAGGT ATTCCACTGC GTTCATCGCC GCCGGGTCGA 480
TCCAGCCGGT ACCGGTGGGC GTCACCAGCA CCAGCACCGA TCGCTCGAAG GCGCCGCTGC 540

GCTGCAGCTC GCGCAAGGCC AGACGCGCCC GCTGGCGCGG GGTCTCTGCC GCGCGCAGAC 600
CGACGTAGAC GCGAATCGGC TCGAGCGCCG AGCGGCCGCT CAAGACGCTG ATATCCGCCG 660
CCGACGGGCC GGAGCCGATG AACTCGCGGC CGGTGCGGCC CAGCTCCTCC CAGCGCAGCA 720
ACGAGGCCCG GCTGCCGCTT TTCAGCGGCG AGGCCGGTGG CGCCGTCTCC GGTTCGATCA 780
GGGCGTCGTA CTGCGCGAAG GATGCGTCCA GCATGCGCAG TGCCCGCGCC GCCAGCACAT 840
CGCTGAGCAG CGACCAGAAC AGCGCCAGCG CCACCAGCAC GCCGATCACG TTGGCCAGGC 900
GCCGTGGCAG CACGCGGTCG GCGTGCCGCG AGACGAAGCG CGACACCAGC CGATACAGAC 960
GCGCCAGCGT CAGCAGGATG AGAAAGGTCG CCAGCGCGGT GAGAATGACT TCGAGCAGGT 1020
GCGCACTGCT CACCGGCGGC ATGCCCATCA GCGCGCGTAC CGCGTTCTGC CAGCCGGCGA 1080
CCTGGCTGAG GAAATACCCG GCCAGCAGCA GGCAGCCGAC CGCGATCAGC AGATTGACCC 1140
GCTCGCGCTG CCAGCCTGGG CGCTCCGGCA GTTCCAGATA GCGCCACAGC CAGCGCCAGA 1200
ACACGCCGAG GCCATAGCCC ACCGCCAGCG CCGCGCCGGC CAGCACGCCC TGGCTCAGCG 1260
TCGAGCGCGG CAGCAGCGAT GGCGTCAGCG CCGCGCAGAA GAACAGCGTG CCCAGCAGCA 1320
GGCCGAAACC GGACAGCGAG CGCCAGATAT AGAGGACGGG CAGGTGCAGC ATGAAGATCT 1380
CCGCGGTCGG GTGACGGCGT CGCGCCTCGG CATATCGAGG CGTGTCCGGT CGTGCGGTTC 1440
CCGTGATGGT CCGCAGCAGG CCAATCCGAT GCAACGATGG CCGAGCGGCC GACTCAAACG 1500
TCTACATTTC CCTAGTGCTG CCGGAACCGA TCGCCG 1536

ATG AGC ATC CCA GAC AAC ACC TAT ATC GAA TGG CTG GTC AGC CAG TCC 1584
Met Ser Ile Pro Asp Asn Thr Tyr Ile Glu Trp Leu Val Ser Gln Ser

ATG CTG CAT GCG GCC CGC GAG CGG TCG CGT CAT TAC GCC GGC CAG GCG 1632
Met Leu His Ala Ala Arg Glu Arg Ser Arg His Tyr Ala Gly Gln Ala

CGT CTC TGG CAG CGG CCT TAT GCC CAG GCC CGC CCG CGC GAT GCC AGC 1680
Arg Leu Trp Gln Arg Pro Try Ala Gln Ala Arg Pro Arg Asp Ala Ser

GCC ATC GCC TCG GTG TGG TTC ACC GCC TAT CCG GCG GCC ATC ATC ACG 1728
Ala Ile Ala Ser Val Trp Phe Thr Ala Tyr Pro Ala Ala Ile Ile Thr

CCG GAA GGC GGC ACG GTA CTC GAG GCC CTC GGC GAC GAC CGC CTC TGG 1776
Pro Glu Gly Gly Thr Val Leu Glu Ala Leu Gly Asp Asp Arg Leu Trp

AGT GCG CTC TCC GAA CTC GGC GTG CAG GGC ATC CAC AAC GGG CCG ATG 1824
Ser Ala Leu Ser Glu Leu Gly Val Gln Gly Ile His Asn Gly Pro Met

AAG CGT TCC GGT GGC CTG CGC GGA CGC GAG TTC ACC CCG ACC ATC GAC 1872
Lys Arg Ser Gly Gly Leu Arg Gly Arg Glu Phe Thr Pro Thr Ile Asp

GGC AAC TTC GAC CGC ATC AGC TTC GAT ATC GAC CCG AGC CTG GGG ACC 1920
Gly Asn Phe Asp Arg Ile Ser Phe Asp Ile Asp Pro Ser Leu Gly Thr

GAG GAG CAG ATG CTG CAG CTC AGC CGG GTG GCC GCG GCG CAC AAC GCC 1968
Glu Glu Gln Met Leu Gln Leu Ser Arg Val Ala Ala Ala His Asn Ala

ATC GTC ATC GAC GAC ATC GTG CCG GCA CAC ACC GGC AAG GGT GCC GAC 2016
Ile Val Ile Asp Asp Ile Val Pro Ala His Thr Gly Lys Gly Ala Asp

TTC CGC CTC GCG GAA ATG GCC TAT GGC GAC TAC CCC GGG CTG TAC CAC 2064
Phe Arg Leu Ala Glu Met Ala Tyr Gly Asp Tyr Pro Gly Leu Tyr His

ATG GTG GAA ATC CGC GAG GAG GAC TGG GAG CTG CTG CCC GAG GTG CCG 2112
Met Val Glu Ile Arg Glu Glu Asp Trp Glu Leu Leu Pro Glu Val Pro

GCC GGG CGT GAT TCG GTC AAC CTG CTG CCG CCG GTG GTC GAC CGG CTC 2160
Ala Gly Arg Asp Ser Val Asn Leu Leu Pro Pro Val Val Asp Arg Leu

AAG GAA AAG CAC TAC ATC GTC GGC CAG CTG CAG CGG GTG ATC TTC TTC 2208
Lys Glu Lys His Tyr Ile Val Gly Gln Leu Gln Arg Val Ile Phe Phe

GAG CCG GGC ATC AAG GAC ACC GAC TGG AGC GTC ACC GGC GAG GTC ACC 2256
Glu Pro Gly Ile Lys Asp Thr Asp Trp Ser Val Thr Gly Glu Val Thr

GGG GTC GAC GGC AAG GTG CGT CGC TGG GTC TAT CTG CAC TAC TTC AAG 2304
Gly Val Asp Gly Lys Val Arg Arg Trp Val Tyr Leu His Tyr Phe Lys

GAG GGC CAG CCG TCG CTG AAC TGG CTC GAC CCG ACC TTC GCC GCG CAG 2352
Glu Gly Gln Pro Ser Leu Asn Trp Leu Asp Pro Thr Phe Ala Ala Gln

CAG CTG ATC ATC GGC GAT GCG CTG CAC GCC ATC GAC GTC ACC GGC GCC 2400
Gln Leu Ile Ile Gly Asp Ala Leu His Ala Ile Asp Val Thr Gly Ala

CGG GTG CTG CGC CTG GAC GCC AAC GGC TTC CTC GGC GTG GAA CGG CGC 2448
Arg Val Leu Arg Leu Asp Ala Asn Gly Phe Leu Gly Val Glu Arg Arg

GCC GAG GGC ACG GCC TGG TCG GAG GGC CAC CCG CTG TCC GTC ACC GGC 2496
Ala Glu Gly Thr Ala Trp Ser Glu Gly His Pro Leu Ser Val Thr Gly

AAC CAG CTG CTC GCC GGG GCG ATC CGC AAG GCC GGC GGC TTC AGC TTC 2544
Asn Gln Leu Leu Ala Gly Ala Ile Arg Lys Ala Gly Gly Phe Ser Phe

CAG GAG CTG AAC CTG ACC ATC GAT GAC ATC GCC GCC ATG TCC CAC GGC 2592
Gln Glu Leu Asn Leu Thr Ile Asp Asp Ile Ala Ala Met Ser His Gly

GGG GCC GAT CTG TCC TAC GAC TTC ATC ACC CGC CCG GCC TAT CAC CAT 2640
Gly Ala Asp Leu Ser Tyr Asp Phe Ile Thr Arg Pro Ala Tyr His His

GCG TTG CTC ACC GGC GAT ACC GAA TTC CTG CGC ATG ATG CTG CGC GAA 2688
Ala Leu Leu Thr Gly Asp Thr Glu Phe Leu Arg Met Met Leu Arg Glu

GTG CAC GCC TTC GGC ATC GAC CCG GCG TCA CTG ATC CAT GCG CTG CAG 2736
Val His Ala Phe Gly Ile Asp Pro Ala Ser Leu Ile His Ala Leu Gln

AAC CAT GAC GAG TTG ACC CTG GAG CTG GTG CAC TTC TGG ACG CTG CAC 2784
Asn His Asp Glu Leu Thr Leu Glu Leu Val His Phe Trp Thr Leu His

GCC TAC GAC CAT TAC CAC TAC AAG GGC CAG ACC CTG CCC GGC GGC CAC 2832
Ala Tyr Asp His Tyr His Tyr Lys Gly Gln Thr Leu Pro Gly Gly His

CTG CGC GAA CAT ATC CGC GAG GAA ATG TAC GAG CGG CTG ACC GGC GAA 2880
Leu Arg Glu His Ile Arg Glu Glu Met Tyr Glu Arg Leu Thr Gly Glu

CAC GCG CCG TAC AAC CTC AAG TTC GTC ACC AAC GGG GTG TCC TGC ACC 2928
His Ala Pro Tyr Asn Leu Lys Phe Val Thr Asn Gly Val Ser Cys Thr

ACC GCC AGC GTG ATC GCC GCG GCG CTT AAC ATC CGT GAT CTG GAC GCC 2976
Thr Ala Ser Val Ile Ala Ala Ala Leu Asn Ile Arg Asp Leu Asp Ala

ATC GGC CCG GCC GAG GTG GAG CAG ATC CAG CGT CTG CAT ATC CTG CTG 3024
Ile Gly Pro Ala Glu Val Glu Gln Ile Gln Arg Leu His Ile Leu Leu

GTG ATG TTC AAT GCC ATG CAG CCC GGC GTG TTC GCC CTC TCC GGC TGG 3072
Val Met Phe Asn Ala Met Gln Pro Gly Val Phe Ala Leu Ser Gly Trp

GAT CTG GTC GGC GCC CTG CCG CTG GCG CCC GAG CAG GTC GAG CAC CTG 3120
Asp Leu Val Gly Ala Leu Pro Leu Ala Pro Glu Gln Val Glu His Leu

ATG GGC GAT GGC GAT ACC CGC TGG ATC AAT CGC GGC GGC TAT GAC CTC 3168
Met Gly Asp Gly Asp Thr Arg Trp Ile Asn Arg Gly Gly Tyr Asp Leu

GCC GAT CTG GCG CCG GAG GCG TCG GTC TCC GCC GAA GGC CTG CCC AAG 3216
Ala Asp Leu Ala Pro Glu Ala Ser Val Ser Ala Glu Gly Leu Pro Lys

GCC CGC TCG CTG TAC GGC AGC CTG GCC GAG CAG CTG CAG CGG CCA GGC 3264
Ala Arg Ser Leu Tyr Gly Ser Leu Ala Glu Gln Leu Gln Arg Pro Gly

TCC TTC GCC TGC CAG CTC AAG CGC ATC CTC AGC GTG CGC CAG GCC TAC 3312
Ser Phe Ala Cys Gln Leu Lys Arg Ile Leu Ser Val Arg Gln Ala Tyr

GAC ATC GCT GCC AGC AAG CAG ATC CTG ATT CCG GAT GTG CAG GCG CCG 3360
Asp Ile Ala Ala Ser Lys Gln Ile Leu Ile Pro Asp Val Gln Ala Pro

GGA CTC CTG GTG ATG GTC CAC GAG CTG CCT GCC GGC AAG GGC GTG CAG 3408
Gly Leu Leu Val Met Val His Glu Leu Pro Ala Gly Lys Gly Val Gln

CTC ACG GCA CTG AAC TTC AGC GCC GAG CCG GTC AGC GAG ACC ATC TGC 3456
Leu Thr Ala Leu Asn Phe Ser Ala Glu Pro Val Ser Glu Thr Ile Cys

CTG CCC GGC GTG GCG CCC GGC CCG GTG GTG GAC ATC ATT CAC GAG AGT 3504
Leu Pro Gly Val Ala Pro Gly Pro Val Val Asp Ile Ile His Glu Ser

GTG GAG GGC GAC CTC ACC GAC AAC TGC GAG CTG CAG ATC AAC CTC GAC 3552
Val Glu Gly Asp Leu Thr Asp Asn Cys Glu Leu Gln Ile Asn Leu Asp

CCG TAC GAG GGG CTT GCC CTG CGT GTG GTG AGC GCC GCG CCG CCG GTG 3600
Pro Tyr Glu Gly Leu Ala Leu Arg Val Val Ser Ala Ala Pro Pro Val

ATC TGA GCGC 3610
Ile

CCTCTTCGCG CGCCCCGGGT CCGCCGCTAT AGTGCGCAGC GCCTGGGGCG CGCATTGCCC 3670
TCGCCGTCGA GACCAGCCCG TGTCGTTCAC TTCGCTTTTC CGCCTTGCGC TGCTGCCGCT 3730
GGCGCTGCTT GCCGCACCCG TCTGGGCGCA GACCGCCTGC CCGCCCGGCC AGCAGCCGAT 3790
CTGCCTGAGC GGCAGCTGCC TCTGCGTGCC GGCCGCCGCC AGCGATCCAC AGGCGGTCTA 3850
CGACCGCGTG CAGCGTATGG CTACGCTGGC CCTGCAGAAC TGGATCCAGC AGTCGCGCGA 3910
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GTATTTCGAT CTTGCCGTGC TGGAGAGTGC GCGGTACCGC GTCGGCGACG AGGTGGTGCT 4030
GACTGCCGGC AACACCCTGC TGCGCAACCC GGACGTCAAT GCCGTGACCC TGATCGACGT 4090
CATCGTCTTC CGCCACGAGG AGGATGCCCG GGACAACGTC GCGCTCTGGG CCCATGAGCT 4150
CAAGCACGTC GAGCAATATC TGGACTGGGG CGTCGCCGAG TTCGCCCGGC GCTATACGCA 4210
GGATTTCCGT GCCGTGGAGC GCCCGGCCTA TGCGCTGGAG CGTGAGGTGG AAGAGGCCCT 4270
GCGCGAGACG CAGACGCGGC GCTGAGCGAG CTGATCGGTG CTGCTGCCCG CACTGGGCTG 4330
AAGCCCACCA ATGACGCCGG CGAAAACGAA AAACCCCGCC GAGGCGGGGT TTCTGACGCG 4390
GGTTGTGCGG TCAGCTCAGA ACGCCGGGAC CACGGCGCCC TTGTACTTTT CCTCGATGAA 4450
CTGGCGTACT TGCTCGCTGT GCAGCGCGGC AGCCAGTTTC TGCATGGCAT CGCTGTCCTT 4510
GTTGTCCGGA CGGGCGACCA GAATGTTCAC GTATGGCGAG TCGCTGCCCT CGATCACCAG 4570
GGCGTCCTGG GTCGGGTTCA GCTTGGCTTC CAGCGCGTAG TTGGTGTTGA TCAGCGCCAG 4630
GTCGACCTGG GTCAGCACGC GCGGCAGAGT CGCGGCTTCC AGTTCGCGGA TCTTGATCTT 4690
CTTCGGGTTC TCGGCGATGT CTTCGGCGTG GCGGTGATGC CGGCGCCGTC CTTCAGACCG 4750
ATC 4753